Sujit Silas Armstrong Suthahar

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EDUCATION

University of California, Los Angeles   Los Angeles, CA
M.S. Bioengineering   *September 2023 – Present*
GPA: 3.97/4.00

University of California, Riverside   Riverside, CA
B.S. Biology, Honors   *March 2021*
GPA: 3.60/4.00

RESEARCH EXPERIENCE

University of California, Los Angeles   Los Angeles, CA
Graduate Student Researcher (GSR); Advisor: Dr. Patrick Allard   *September 2023 – Present*

- Led comprehensive multi-omics data analyses (RRBS, WGBS, ATAC-seq, RNA-seq) to elucidate the epigenetic effects of environmental toxins, particularly arsenic, making significant contributions to the emerging field of toxicoepigenetics.
- Developed and maintained a versatile suite of Python, Bash, and R scripts for diverse analyses and automated pipelines.
- Designed and implemented NextFlow pipelines optimized for both local and distributed computing environments, enhancing reproducibility and scalability of bioinformatics workflows.
- Created a user-friendly HTML-based custom bash script generator specifically for nf-core pipelines, empowering non-expert users to effortlessly submit and manage their jobs on high-performance computing clusters.

University of California, Los Angeles   Los Angeles, CA
Researcher; Advisor: Dr. William Speier   *September 2023 – Present*

- Designed and implemented a Multiple Instance Learning (MIL) deep learning model for thyroid nodule classification, boosting accuracy by 11% and enhancing diagnostic precision for indeterminate cases.
- Leveraged CUDA architecture to optimize and accelerate deep learning model training on GPUs within a High-Performance Computing (HPC) environment, significantly reducing processing time and improving model iteration speed.
- Developed an advanced U-Net classifier featuring enhanced skip connections and integrated image preprocessing techniques to achieving precise needle segmentation in medical imaging.
- Streamlined the training-validation workflow by automating processes on an HPC cluster, enabling efficient GPU-accelerated training at scale.

La Jolla Institute for Immunology   San Diego, CA
Research Associate II; Advisor: Klaus Ley, MD   *June 2021 – July 2023*

- Conducted comprehensive analysis of clinical NGS data and diverse databases to assess risks associated with atherosclerosis, diabetes, or HIV thereby improving disease profile understanding and supporting biomarker analysis in clinical studies.
- Managed and executed routine bioinformatics tasks, including running mapping and QC pipelines on both local and HPC environments, providing robust data analysis support, and maintaining data integrity across multiple projects.

University of California, Riverside   Riverside, CA
Research Assistant (RA); Advisor: Dr. Martín I. García-Castro   October 2019 – June 2021

- Conducted in-depth mRNA transcriptome analysis using R and Python, spearheading an independent research project comparing hESC transcriptomes of differentiating neural crest and ectodermal cells.
- Employed advanced protein modeling tools including Pymol, I-Tasser, PSIPRED, Robetta, and SAVES 6.0 to elucidate DNA-transcription factor (TF) interactions in early development, integrating molecular biology knowledge with computational approaches to gain novel insights.

PROFESSIONAL EXPERIENCE

GRAIL   Menlo Park, CA
Computational Biology & Machine Learning Intern   *June 2024 – September 2024*

- Jointly optimized classifier features and assay probes, laying the groundwork for a novel false positive analysis, increasing cfDNA detection sensitivity for a few early-stage cancer types by 8%.
- Designed and developed a cross functional annotation toolkit in a CI/CD environment that helps annotate DMRs and with respect to targeted panel regions and genome annotations optimizing feature selection process reducing non-specific features.
- Refactored functions, updated pipelines, and successfully landed two merge requests related to the development of two vignettes and the false positive analysis workflow.

La Jolla Institute for Immunology   San Diego, CA
Bioinformatics Specialist   *June 2021 – July 2023*

- Statistically analyzed single-cell RNA-seq, RNA-seq, and CITE-seq data of peripheral blood mononuclear cell (PBMC) samples, using dimensionality reduction algorithms, and other R/Python packages.
- Automated data visualization workflows and developed data preprocessing pipelines for scRNA-seq and RNA-seq data, significantly enhancing efficiency and reproducibility in high-throughput genomic data analysis.
- Developed and applied a computational method to validate and optimize antibody titration concentrations for a panel of 124 antibodies used in CITE-seq experiments, improving the accuracy and reliability of multi-omics data integration.
- Designed and implemented a novel statistical pipeline to analyze T-cell receptor (TCR) repertoire diversity and clonality from TCR sequencing data, contributing to advancements in immunogenomics research.

LEADERSHIP EXPERIENCE

Highlander Union   Riverside, CA
HUB Associate   *September 2018 – July 2020*

- Fostered student success by facilitating access to campus resources, exemplifying a student-centric approach to service.
- Managed space reservations and event coordination, contributing to a vibrant campus community life.
- Collaborated with professional staff to enhance the university's social and recreational offerings, promoting teamwork.

Danish Display   Tamil Nadu, India
Marketing Director   *August 2020 – January 2021*

- Conceptualized and executed a brand re-design, elevating product, and store appeal, driving a 30% increase in revenue.
- Promoted digital marketing efforts, including website optimization and social media engagement, achieving a 46% growth in followers, and improving business visibility.
- Fostered partnerships with influencers and integrated analytic tools to refine marketing campaigns, demonstrating a keen aptitude for brand promotion and business growth.

SKILLS

Programming: Proficient in Python, R, Bash/Shell, Go, SQL, JavaScript, C/C++, CSS/HTML, and LaTex
Software: MS Word, PowerPoint, Excel, Pymol, Linux, Blender, AutoCAD, IBM SPSS, SAS/STAT, Docker, Git
Machine Learning / Deep Learning: TensorFlow, Keras, PyTorch, Scikit-learn, CUDA
Bioinformatics Tools: STAR aligner, DESeq2, Cell Ranger, Seurat, Scanpy, NextFlow, Seven Bridges, PyMol, BioPython, Bioconductor, PSIPRED, DeepFold, edgeR, dplyr, tidyr, ggplot2, complex heatmaps, seaborn, WGCNA, MiXCR, etc.

AWARDS & PROFESSIONAL ASSOCIATIONS

Awards: UCLA Graduate Student Researcher, American Association of Immunologists Travel Award, Highlander Union Excellence Award, UCR Achievement Scholarship

Professional Associations: American Association of Immunologists - *Member,* Graduate Faculty Executive Commission UCLA - *Samueli School of Engineering Representative,* UCLA Venture Accelerator - *Member*

PUBLICATIONS

Armstrong Suthahar SS, Nettersheim FS, Alimadadi A, Wang E, Billitti M, Resto-Trujillo N, Roy P, Hedrick CC, Ley K, Orecchioni M. Olfr2-positive macrophages originate from monocytes proliferate in situ and present a pro-inflammatory foamy-like phenotype. Cardiovasc Res. 2024 Sep 4:cvae153. doi: 10.1093/cvr/cvae153. Epub ahead of print. PMID: 39229899.

Armstrong, S. S., Nettersheim, F. S., Durant, C., Blanco-Dominguez, R., Roy, P., Orecchioni, M., Suryawanshi, V., & Ley, K. (2022). Titration of 124 antibodies using CITE-Seq on human PBMCs. *Scientific Reports*, *12*(1), Article 1.

Armstrong, S. S., Chen, D. G., Kumar, S., Heath, J. R., Feinstein, M. J., Greenland, J. R., Calabrese, D. R., Lanier, L. L., Ley, K., & Shemesh, A. (2024). CITE-seq analysis reveals human cytomegalovirus and diabetes-associated adaptive NK cell alterations in cardiovascular disease. bioRxiv, 2024.03.22.581997.

Armstrong Suthahar, S. S., ROY, P., Makings, J., & Ley, K. (2023). Identification of apolipoprotein B-reactive CDR3 motifs allow tracking of atherosclerosisrelated memory CD4+ T cells in multiple donors. *Frontiers in Immunology*, *15*, 1302031.

Armstrong Suthahar, S. S. (2021). *A comparative transcriptomic analysis of differentiating neural crest cells and neuroectoderm or ectoderm cells at early development.*

Freuchet, **Armstrong, S. S.**, A., Roy, P., Oliaeimotlagh, M., Kumar, S., Orecchioni, M., Ali, A. J., Khan, A., Makings, J., Lyu, Q., Winkels, H., Wang, E., Durant, C., Ghosheh, Y., Gulati, R., Nettersheim, F., & Ley, K. (2023). Identification of human exTreg cells as CD16+CD56+ cytotoxic CD4+ T cells. *Nature Immunology*, *24*(10), 1748–1761.

Athreya, S., Melehy, A., **Armstrong Suthahar, S. S**., Ivezić, V., Radhachandran, A., Sant, V., ... & Speier, W. (2024). Reducing Overtreatment of Indeterminate Thyroid Nodules Using a Multimodal Deep Learning Model. arXiv preprint arXiv:2409.19171.

Saigusa, R., Vallejo, J., Gulati, R., **Armstrong Suthahar, S. S.,** *Suryawanshi, V., Alimadadi, A., Makings, J., Durant, C. P., Freuchet, A., Roy, P., Ghosheh, Y., Pandori, W., Pattarabanjird, T., Drago, F., Taylor, A., McNamara, C. A., Shemesh, A., Lanier, L. L., Hedrick, C. C., & Ley, K. (2022). Sex Differences in Coronary Artery Disease and Diabetes Revealed by scRNA-Seq and CITE-Seq of Human CD4+ T Cells. International Journal of Molecular Sciences, 23(17), Article 17.*

Vallejo, J., Saigusa, R., Gulati, R., **Armstrong Suthahar, S. S.,** Suryawanshi, V., Alimadadi, A., Durant, C. P., Ghosheh, Y., Roy, P., Ehinger, E., Pattarabanjird, T., Hanna, D. B., Landay, A. L., Tracy, R. P., Lazar, J. M., Mack, W. J., Weber, K. M., Adimora, A. A., Hodis, H. N., ... Ley, K. (2022). Combined protein and transcript single-cell RNA sequencing in human peripheral blood mononuclear cells. *BMC Biology*, *20*(1), 193.

Iqneibi S, Saigusa R, Khan A, Oliaeimotlagh M, **Armstrong Suthahar SS**, Kumar S, Alimadadi A, Durant CP, Ghosheh Y, McNamara CA, Hedrick CC and Ley K (2023) Single cell transcriptomics reveals recent CD8T cell receptor signaling in patients with coronary artery disease. *Front. Immunol.* 14:1239148. doi: 10.3389/fimmu.2023.123914

Saigusa, R., Roy, P., Freuchet, A., Gulati, R., Ghosheh, Y., **Armstrong Suthahar, S. S.,** Durant, C. P., Hanna, D. B., Kiosses, W. B., Orecchioni, M., Wen, L., Wu, R., Kuniholm, M. H., Landay, A. L., Anastos, K., Tien, P. C., Gange, S. J., Kassaye, S., Vallejo, J., Ley, K. (2022). Single cell transcriptomics and TCR reconstruction reveal CD4 T cell response to MHC-II-restricted APOB epitope in human cardiovascular disease. *Nature Cardiovascular Research*, Article 5.

Roy, P., Sidney, J., Lindestam Arlehamn, C. S., Phillips, E., Mallal, S., **Armstrong Suthahar, S. S.,** Billitti, M., Rubiro, P., Marrama, D., Drago, F., Vallejo, J., Suryawanshi, V., Orecchioni, M., Makings, J., Kim, P. J., McNamara, C. A., Peters, B., Sette, A., & Ley, K. (2022). Immunodominant MHC-II (Major Histocompatibility Complex II) Restricted Epitopes in Human Apolipoprotein B. *Circulation Research*, *131*(3), 258–276.

Wen, L., Marki, A., Wang, Z., Orecchioni, M., Makings, J., Billitti, M., Wang, E., **Armstrong Suthahar, S. S.,** Kim, K., Kiosses, W. B., Mikulski, Z., & Ley, K. (2022). A humanized β2 integrin knockin mouse reveals localized intra- and extravascular neutrophil integrin activation in vivo. *Cell Reports*, *39*(9), 110876.

Nettersheim, F. S., Winkels, H., Kobiyama, K., Durant, C., **Armstrong, S. S.,** Brunel, S., Roy, P., Dileepan, T., & Jenkins, M. K. (2023). Single-cell transcriptomes and T cell receptors of vaccine-expanded apolipoprotein B-specific T cells. *Frontiers in Cardiovascular Medicine*, *9*, 1076808.

ABSTRACTS AND PRESENTATIONS

scRNA-Seq with CITE-Seq reveals differential surface marker and gene expression in natural killer cells from subjects with and without coronary artery disease, February 2023 American Association of Immunology Conference – abstract.

A comparative transcriptomic analysis of differentiating neural crest cells and neuroectoderm or ectoderm cells at early development, March 2021, UCR Undergraduate Research Symposium – abstract, and presentation.

Wasserstein cycle-consistent generative adversarial network for RNA-seq and scRNA-seq translation, UCLA Bioengineering Conference 2024 – abstract, and poster presentation.

Single Cell RNA Sequencing Signature of Cardiac Allograft Vasculopathy. Circulation, 148, A12560 - abstract.

Enhancing thyroid cancer diagnosis of indeterminate nodules through multi-modal analysis of ultrasound images, UCLA Jonsson Comprehensive Cancer Center Annual All-Center Symposium 2024 – abstract and poster.

PROJECTS

- Inferring survival benefit of liver transplant in mechanically ventilated patients using feature optimization techniques and machine learning models.
- Support vector machine model for deconvolving and characterizing novel immune cell types in scRNA-seq data.
- tcrDiff – R package for differential T-cell receptor motif analysis.
- R Shiny app for scRNA-seq and RNA-seq data visualization.
- Using machine learning algorithms to predict heart failure based on clinical records.
- U-Net based deep learning model for lung biopsy needle segmentation in CT-scans.

RELEVANT COURSEWORK

- Linear Algebra: Theory and Implementation in Code
- Signal and Image Processing (M209)
- Medical Programming Laboratory (Computer Vision) (M223A)
- Medical Information Infrastructures and Internet Technologies (M227)
- Medical Decision Making - Advanced Statistical Methods (M228)
- Medtech Innovation I: Entrepreneurial Opportunities in Medical Technology (M233A)
- Principles of Magnetic Resonance Imaging (M219)
- Medical Knowledge Represent (Data Structures) (M226)
- Advanced Imaging Informatics (Computer Vision, NLP, Probabilistic IR) (M224B)
- Introduction to Molecular Imaging (M248)
- Machine Learning and Data Driven Modeling (M275)
- Deterministic Models in Biology (BIOMATH 201)

REFERENCES

- Dr. Alexis Thornton, PhD, ML/Computational Biology Data Scientist, GRAIL - athornton@grailbio.com
- Dr. Patrick Allard, PhD, Professor, UCLA Institute for Society and Genetics - pallard@ucla.edu, +1(310)-825-5257
- Dr. Klaus Ley, MD, Co-Director, IMMCG, Medical College of Georgia - kley@augusta.edu, +1(858)-472-7253
- Dr. Martín I. García-Castro, Full Professor, Biomedical Sciences - martin.garcia-castro@ucr.edu, +1 (951) 827-7251